

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Lal, Preeti
Corley, Neil C.
Tang, Y. Tom
- (ii) TITLE OF THE INVENTION: AUTOANTIGEN-LIKE PROTEIN
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0385 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-855-0555
 - (B) TELEFAX: 650-845-4166
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 395 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: HUVENOB01
 - (B) CLONE: 35842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Phe	Pro	Arg	Val	Ser	Thr	Phe	Leu	Pro	Leu	Arg	Pro	Leu	Ser	Arg
1				5					10					15	
His	Pro	Leu	Ser	Ser	Gly	Ser	Pro	Glu	Thr	Ser	Ala	Ala	Ala	Ile	Met
			20					25					30		
Leu	Leu	Thr	Val	Arg	His	Gly	Thr	Val	Arg	Tyr	Arg	Ser	Ser	Ala	Leu
		35				40						45			
Leu	Ala	Arg	Thr	Lys	Asn	Asn	Ile	Gln	Arg	Tyr	Phe	Gly	Thr	Asn	Ser
	50					55					60				
Val	Ile	Cys	Ser	Lys	Lys	Asp	Lys	Gln	Ser	Val	Arg	Thr	Glu	Glu	Thr
65					70					75				80	
Ser	Lys	Glu	Thr	Ser	Glu	Ser	Gln	Asp	Ser	Glu	Lys	Glu	Asn	Thr	Lys
			85						90					95	
Lys	Asp	Leu	Leu	Gly	Ile	Ile	Lys	Gly	Met	Lys	Val	Glu	Leu	Ser	Thr
		100						105					110		
Val	Asn	Val	Arg	Thr	Thr	Lys	Pro	Pro	Lys	Arg	Arg	Pro	Leu	Lys	Ser
		115					120					125			
Leu	Glu	Ala	Thr	Leu	Gly	Arg	Leu	Arg	Arg	Ala	Thr	Glu	Tyr	Ala	Pro
	130				135					140					
Lys	Lys	Arg	Ile	Glu	Pro	Leu	Ser	Pro	Glu	Leu	Val	Ala	Ala	Ala	Ser
145					150					155					160
Ala	Val	Ala	Asp	Ser	Leu	Pro	Phe	Asp	Lys	Gln	Thr	Thr	Lys	Ser	Glu
			165					170						175	
Leu	Leu	Ser	Gln	Leu	Gln	Gln	His	Glu	Glu	Glu	Ser	Arg	Ala	Gln	Arg
		180						185					190		
Asp	Ala	Lys	Arg	Pro	Lys	Ile	Ser	Phe	Ser	Asn	Ile	Ile	Ser	Asp	Met
		195					200					205			
Lys	Val	Ala	Arg	Ser	Ala	Thr	Ala	Arg	Val	Arg	Ser	Arg	Pro	Glu	Leu
	210					215					220				
Arg	Ile	Gln	Phe	Asp	Glu	Gly	Tyr	Asp	Asn	Tyr	Pro	Gly	Gln	Glu	Lys
225					230					235					240
Thr	Asp	Asp	Leu	Lys	Lys	Arg	Lys	Asn	Ile	Phe	Thr	Gly	Lys	Arg	Leu
			245					250						255	
Asn	Ile	Phe	Asp	Met	Met	Ala	Val	Thr	Lys	Glu	Ala	Pro	Glu	Thr	Asp
		260						265					270		
Thr	Ser	Pro	Ser	Leu	Trp	Asp	Val	Glu	Phe	Ala	Lys	Gln	Leu	Ala	Thr
		275					280					285			
Val	Asn	Glu	Gln	Pro	Leu	Gln	Asn	Gly	Phe	Glu	Glu	Leu	Ile	Gln	Trp
	290					295					300				
Thr	Lys	Glu	Gly	Lys	Leu	Trp	Glu	Phe	Pro	Ile	Asn	Asn	Glu	Ala	Gly
305					310					315					320
Phe	Asp	Asp	Asp	Gly	Ser	Glu	Phe	His	Glu	His	Ile	Phe	Leu	Glu	Lys
			325					330					335		
His	Leu	Glu	Ser	Phe	Pro	Lys	Gln	Gly	Pro	Ile	Arg	His	Phe	Met	Glu
			340					345					350		
Leu	Val	Thr	Cys	Gly	Leu	Ser	Lys	Asn	Pro	Tyr	Leu	Ser	Val	Lys	Gln
		355					360					365			
Lys	Val	Glu	His	Ile	Glu	Trp	Phe	Arg	Asn	Tyr	Phe	Asn	Glu	Lys	Lys
	370					375					380				
Asp	Ile	Leu	Lys	Glu	Ser	Asn	Ile	Gln	Phe	Asn					
385						390				395					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: HUVENOB01
 (B) CLONE: 35842

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GACGTGTTTG	GCAGCGGGAC	GCACCATTTT	AGTTGTGTTC	TTGGTTCATT	TCGTGTCTCG	60
GCGATGTTTC	CTAGAGTCTC	GACGTTCCTA	CCTCTTCGCC	CCCTTTCCCG	CCACCCTTTG	120
TCCTCTGGAA	GCCCGGAGAC	ATCAGCGGCT	GCGATTATGC	TACTCACTGT	TCGGCACGGA	180
ACAGTCAGGT	ACCGCAGTTC	AGCGCTGTTG	GCCCGGACAA	AAAATAACAT	CCAAAGATAT	240
TTTGGCACTA	ACAGTGTGAT	CTGTAGCAAG	AAAGATAAGC	AGTCTGTTTC	AACTGAGGAG	300
ACTTCCAAGG	AGACTTCAGA	GAGCCAAGAC	AGTGAAAAGG	AAAATACGAA	AAAAGACTTG	360
TTAGGCATTA	TTAAGGGCAT	GAAAGTTGAA	TTAAGCACAG	TAAATGTACG	AACAACAAAG	420
CCCCCAAAA	GAAGACCACT	TAAAAGTTTG	GAAGCTACAC	TTGGCAGGCT	TCGAAGAGCT	480
ACAGAATATG	CTCCAAAGAA	GAGAATTGAG	CCCCTGAGTC	CTGAGTTGGT	GGCAGCTGCA	540
TCTGCTGTGG	CAGATTCTCT	CCCTTTTGAT	AAGCAAAACA	CCAAGTCAGA	GCTGCTGAGC	600
CAGCTCCAGC	AGCATGAGGA	AGAGTCAAGG	GCACAGAGAG	ATGCAAAGCG	ACCTAAAATT	660
AGTTTCAGTA	ACATAATATC	AGATATGAAA	GTTGCCAGAT	CTGCTACAGC	TAGAGTTCGT	720
TCAAGACCAG	AGCTTCGGAT	TCAGTTTGAT	GAAGGCTATG	ACAATTATCC	TGGCCAGGAG	780
AAGACGGATG	ATCTTAAAAA	AAGGAAAAAT	ATATTCACAG	GGAAAAGACT	TAATATTTTT	840
GACATGATGG	CAGTTACTAA	AGAAGCACCT	GAAACAGACA	CATCACCTTC	ACTTTGGGAT	900
GTGGAATTTG	CTAAGCAGTT	AGCCACAGTA	AATGAACAAC	CCCTTCAGAA	TGGATTTGAA	960
GAGCTGATCC	AGTGGACAAA	AGAGGGGAAA	CTATGGGAGT	TCCCAATTAA	CAATGAAGCA	1020
GGTTTTGATG	ATGATGGTTC	AGAATTTTCAT	GAACATATAT	TTCTGGAGAA	ACACCTGGAG	1080
AGCTTTCCAA	AACAAGGACC	AATTCGCCAC	TTCATGGAGC	TGGTGAATTG	TGGCCTTTCC	1140
AAAAACCCAT	ATCTTAGTGT	TAAACAGAAG	GTTGAACACA	TAGAGTGGTT	TAGAAATTAT	1200
TTTAATGAAA	AAAAGGATAT	TCTAAAAGAA	AGTAACATAC	AGTTCAATTA	AGACCATGGA	1260
AATTTTTATT	TCAAACAATT	AGAGATGGAT	ATTACAACATA	AATAAAATAA	TTGC	1314

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: GenBank
 (B) CLONE: 1272669

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Leu	His	Arg	Ile	Pro	Ala	Phe	Leu	Arg	Pro	Arg	Pro	Phe	Ser	Gly
1				5				10						15	
Leu	Pro	Leu	Ser	Cys	Gly	Asn	Arg	Asp	Val	Ser	Val	Ala	Val	Leu	Pro
			20					25					30		
Ala	Ala	Gln	Ser	Gly	Ala	Val	Arg	Thr	Glu	Asn	Asn	Ile	Gln	Arg	His
			35					40					45		
Phe	Cys	Thr	Ser	Arg	Ser	Ile	Cys	Ser	Lys	Lys	Val	Asp	Gln	Ser	Val
			50					55				60			
Pro	Ala	Asn	Glu	Ile	Ser	Gln	Lys	Ala	Ala	Glu	Ser	Gln	Gly	Arg	Gly
65						70				75				80	
Lys	Glu	Thr	Leu	Lys	Lys	Asp	Leu	Leu	Asp	Ile	Ile	Lys	Asp	Met	Lys
				85					90					95	
Val	Asp	Leu	Ser	Thr	Ala	Asn	Val	Lys	Thr	Pro	Lys	Pro	Arg	Gly	Arg
				100					105				110		
Lys	Pro	Ser	Ala	Ser	Leu	Glu	Ala	Thr	Val	Asp	Arg	Leu	Gln	Lys	Ala
				115									125		
Pro	Glu	Asp	Pro	Pro	Lys	Lys	Arg	Asn	Glu	Phe	Leu	Ser	Pro	Glu	Leu

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130		135		140
Val Ala Ala Ala Ser	Ala Val Ala Asp Ser	Leu Pro Phe Asp Lys Gln		
145	150	155		160
Thr Thr Lys Ser Glu	Leu Leu Arg Gln Leu	Gln Gln His Glu Glu Glu		
	165	170		175
Leu Arg Ala Gln Lys	Asp Arg Glu Lys Arg	Arg Arg Ile Ser Phe Thr His		
	180	185		190
Ile Ile Ser Asn Met Lys	Ile Ala Lys Ser Pro	Ser Gly Arg Ala Ser		
	195	200		205
Thr Arg Pro Gln His Gln	Ile Gln Phe Asp Glu	Asp Met Asp Ser Ser		
	210	215		220
Leu Lys Gln Glu Lys Pro	Thr Asp Phe Arg Lys	Arg Lys Tyr Leu Phe		
225	230	235		240
Lys Gly Lys Arg Leu Ser	Ile Phe Ala Asp Lys	Ala Phe Ala Asp Glu		
	245	250		255
Pro Pro Glu Pro Glu Ala	Ser Pro Ser Leu Trp	Glu Ile Glu Phe Ala		
	260	265		270
Lys Gln Leu Ala Ser Val	Ala Asp Gln Pro Phe	Glu Asn Gly Phe Glu		
	275	280		285
Glu Met Ile Gln Trp Thr	Lys Glu Gly Lys Leu	Trp Glu Phe Pro Val		
	290	295		300
Asn Asn Glu Ala Gly Leu	Asp Asp Asp Gly Ser	Glu Phe His Glu His		
305	310	315		320
Ile Phe Leu Asp Lys Tyr	Leu Glu Asp Phe Pro	Lys Gln Gly Pro Ile		
	325	330		335
Arg Leu Phe Met Glu Leu	Val Thr Cys Gly Leu	Ser Lys Asn Pro Tyr		
	340	345		350
Leu Ser Val Lys Gln Lys	Val Glu His Ile Glu	Trp Phe Arg Asn Tyr		
	355	360		365
Phe Asn Glu Lys Arg Asp	Ile Leu Lys Glu Asn	Asn Ile Ala Phe Thr		
370	375	380		